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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/919,932A

DATE: 10/21/2003

TIME: 15:21:11

Input Set : D:\211707US.txt

Output Set: N:\CRF4\10212003\I919932A.raw

3 <110> APPLICANT: MOECKEL, BETTINA
 4 PFEFFERLE, WALTER
 5 HUTHMACHER, KLAUS
 6 RUECKERT, CHRISTIAN
 7 KALINOWSKI, JOERN
 8 PUEHLER, ALFRED
 9 BINDER, MICHAEL
 10 GREISSINGER, DIETER
 11 THIERBACH, GEORG
 13 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METY GENE
 15 <130> FILE REFERENCE: 211707US0X
 17 <140> CURRENT APPLICATION NUMBER: 09/919,932A
 18 <141> CURRENT FILING DATE: 2001-08-02
 20 <150> PRIOR APPLICATION NUMBER: DE 10043334.0
 21 <151> PRIOR FILING DATE: 2000-09-02
 23 <150> PRIOR APPLICATION NUMBER: DE 10109690.9
 24 <151> PRIOR FILING DATE: 2001-02-28
 26 <150> PRIOR APPLICATION NUMBER: US 60/294,252
 27 <151> PRIOR FILING DATE: 2001-05-31
 29 <160> NUMBER OF SEQ ID NOS: 6
 31 <170> SOFTWARE: PatentIn version 3.2
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 1720
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Corynebacterium glutamicum
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 41 <222> LOCATION: (200)..(1510)
 43 <400> SEQUENCE: 1
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 48 gtctattgca atagaccaag ctgttcagta ggggtgcatgg gagaagaatt tcctaataaa 180
 50 aactcttaag gacctccaa atg cca aag tac gac aat tcc aat gct gac cag 232
 51 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln
 52 1 5 10
 54 tgg ggc ttt gaa acc cgc tcc att cac gca ggc cag tca gta gac gca 280
 55 Trp Gly Phe Glu Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala
 56 15 20 25
 58 cag acc agc gca cga aac ctt ccg atc tac caa tcc acc gct ttc gtg 328
 59 Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val
 60 30 35 40
 62 ttc gac tcc gct gag cac gcc aag cag cgt ttc gca ctt gag gat cta 376
 63 Phe Asp Ser Ala Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu

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Input Set : D:\211707US.txt

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67	Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu			
68	60 65 70 75			
70	aac cgc atc gct tcc ctc gaa ggt ggc gtc cac gct gta gcg ttc tcc	472		
71	Asn Arg Ile Ala Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser			
72	80 85 90			
74	tcc gga cag gcc gca acc acc aac gcc att ttg aac ctg gca gga gcg	520		
75	Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala			
76	95 100 105			
78	ggc gac cac atc gtc acc tcc cca cgc ctc tac ggt ggc acc gag act	568		
79	Gly Asp His Ile Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr			
80	110 115 120			
82	cta ttc ctt atc act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg	616		
83	Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val			
84	125 130 135			
86	gaa aac ccc gac gac cct gag tcc tgg cag gca gcc gtt cag cca aac	664		
87	Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn			
88	140 145 150 155			
90	acc aaa gca ttc ttc ggc gag act ttc gcc aac cca cag gca gac gtc	712		
91	Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val			
92	160 165 170			
94	ctg gat att cct gcg gtg gct gaa gtt gcg cac cgc aac agc gtt cca	760		
95	Leu Asp Ile Pro Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro			
96	175 180 185			
98	ctg atc atc gac aac acc atc gct acc gca gcg ctc gtg cgc ccg ctc	808		
99	Leu Ile Ile Asp Asn Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu			
100	190 195 200			
102	gag ctc ggc gca gac gtt gtc gtc gct tcc ctc acc aag ttc tac acc	856		
103	Glu Leu Gly Ala Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr			
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107	Gly Asn Gly Ser Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe			
108	220 225 230 235			
110	gat tgg act gtc gaa aag gat gga aag cca gta ttc ccc tac ttc gtc	952		
111	Asp Trp Thr Val Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val			
112	240 245 250			
114	act cca gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca	1000		
115	Thr Pro Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala			
116	255 260 265			
118	cca gcc ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc	1048		
119	Pro Ala Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly			
120	270 275 280			
122	tcc acc ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac	1096		
123	Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp			
124	285 290 295			
126	acc ctt tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt	1144		
127	Thr Leu Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val			
128	300 305 310 315			

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130 gca gaa ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca      1192
131 Ala Glu Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala
132                               320                               325                               330
134 ggc ctg aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg      1240
135 Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu
136                               335                               340                               345
138 aag tac acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat      1288
139 Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp
140                               350                               355                               360
142 gag gct tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca      1336
143 Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala
144                               365                               370                               375
146 aac atc ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc      1384
147 Asn Ile Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr
148 380                               385                               390                               395
150 cat tca cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag      1432
151 His Ser Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln
152                               400                               405                               410
154 tcc acc gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc      1480
155 Ser Thr Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile
156                               415                               420                               425
158 gct gac ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc      1530
159 Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
160                               430                               435
162 ccagtgcctta aagcgctggg tttttctttt tcagactcgt gagaatgcaa actagactag      1590
164 acagagctgt ccatatacac tggacgaagt tttagtcttg tccaccacaga acaggcggtt      1650
166 attttcatgc ccaccctcgc gccttcaggt caacttgaaa tccaagcgat cggtgatgtc      1710
168 tccaccgaag                                                                1720
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 437
173 <212> TYPE: PRT
174 <213> ORGANISM: Corynebacterium glutamicum
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179 1                               5                               10                               15
182 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
183                               20                               25                               30
186 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
187                               35                               40                               45
190 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
191                               50                               55                               60
194 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
195 65                               70                               75                               80
198 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
199                               85                               90                               95
202 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
203                               100                              105                              110
206 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
207                               115                              120                              125

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210 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
211      130      135      140
214 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
215 145      150      155      160
218 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
219      165      170      175
222 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
223      180      185      190
226 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
227      195      200      205
230 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
231      210      215      220
234 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
235 225      230      235      240
238 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
239      245      250      255
242 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
243      260      265      270
246 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
247      275      280      285
250 Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg
251      290      295      300
254 Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
255 305      310      315      320
258 Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
259      325      330      335
262 Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
263      340      345      350
266 Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
267      355      360      365
270 Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val
271      370      375      380
274 Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
275 385      390      395      400
278 Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
279      405      410      415
282 Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly
283      420      425      430
286 Gly Phe Ala Ala Ile
287      435
290 <210> SEQ ID NO: 3
291 <211> LENGTH: 42
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: synthetic oligonucleotide
298 <400> SEQUENCE: 3
299 ctaataagtc gacaaaggag gacaaccatg ccaaagtacg ac
302 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING

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Input Set : D:\211707US.txt

Output Set: N:\CRF4\10212003\I919932A.raw

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304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: synthetic oligonucleotide
310 <400> SEQUENCE: 4
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314 <210> SEQ ID NO: 5
315 <211> LENGTH: 41
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: synthetic oligonucleotide
322 <400> SEQUENCE: 5
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326 <210> SEQ ID NO: 6
327 <211> LENGTH: 31
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: synthetic oligonucleotide
334 <400> SEQUENCE: 6
335 gtcgtggatc ccctattaga tgtagaactc g 31

VERIFICATION SUMMARY

DATE: 10/21/2003

PATENT APPLICATION: US/09/919,932A

TIME: 15:21:15

Input Set : D:\211707US.txt

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